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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=6; hr=8; min=54; sec=0; ms=423;]

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Reviewer Comments:

<210> 5

<211> 87

<212> PRT

<213> Artificial Sequence

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<223> Xaa = Tyr, Val, Ile, Leu, Met, Phe, Trp

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<223> Xaa = Asn, His, Gln, Cys, Ser, Thr

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<223> Xaa = any amino acid residue

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<223> Xaa = Gly, Ser, Ala, Thr, Pro

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20 25 30
Xaa Xaa Leu Leu Arg Xaa His Xaa Xaa Leu Xaa Xaa Ala Xaa Xaa Arg
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Leu Val Xaa Xaa Xaa Xaa Xaa Leu
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Lys Xaa Xaa Ala Tyr Asp Ala Xaa Asp Xaa Leu Xaa Glu Xaa Glu Xaa
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Xaa Ala Xaa Xaa Xaa Lys Val
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The "<213> Artificial Sequence" needs explanation in a <220>-<223>
section; please give the source of the genetic material. Same error in
Sequences 6-7.

Application No: 10573372 Version No: 3.0

Input Set:

Output Set:

Started: 2009-05-05 15:29:03.484
Finished: 2009-05-05 15:29:15.521
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 37 ms
Total Warnings: 3
Total Errors: 3
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

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<110> Dale, James Langham
Echeverria, Santy Peraza

<130> DAVI172.006APC

<141> 2009-05-05

<151> 2004-09-23

<151> 2003-09-25

<160> 7

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 $\langle 222 \rangle \quad (1) \dots (4323)$

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Gln Thr Leu Leu Asp Lys Ala Ser Asn Cys Ala Ile Gln Gln Leu Ala
20 25 30

cgg cgc cgc ggc ctt cac gat gac ctg agg cgg ctg cgg acg tct ctg 144
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 35 40 45

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Leu Arg Ile His Ala Ile Leu Asp Lys Ala Glu Thr Arg Trp Asn His
50 55 60

aaa aac acg agc ttg gtg gag ctg gtg agg cag ctc aag gat gct gcc 240
Lys Asn Thr Ser Leu Val Glu Leu Val Arg Gln Leu Lys Asp Ala Ala
65 70 75 80

tat gac gcc gag gac tta ctg gag gag ttg gag tac caa gcc gcg aag 288

Tyr Asp Ala Glu Asp Leu Leu Glu Glu Leu Glu Tyr Gln Ala Ala Lys	
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Ser Leu Ser Thr Ala Ser Glu Trp Leu Gly Ala Asp Gly Asp Asp Ala	
115 120 125	
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Gly Thr Arg Leu Arg Glu Ile Gln Gly Lys Leu Cys Asn Ile Ala Ala	
130 135 140	
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Asp Met Met Asp Val Met Gln Leu Leu Ala Pro Asp Asp Gly Gly Arg	
145 150 155 160	
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Gln Phe Asp Trp Lys Val Val Arg Arg Glu Thr Ser Ser Phe Leu Thr	
165 170 175	
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Glu Thr Val Val Phe Gly Arg Asp Gln Glu Arg Glu Lys Val Val Glu	
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210 215 220	
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Tyr Asn Asp Asn Arg Val Gly Asn Tyr Phe His Leu Lys Val Trp Val	
225 230 235 240	
tgt gta tcc gac aat ttc aat gtg aag aga ctg acc aaa gag ata atc	768
Cys Val Ser Asp Asn Phe Asn Val Lys Arg Leu Thr Lys Glu Ile Ile	
245 250 255	
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Glu Ser Ala Thr Lys Val Glu Gln Ser Asp Lys Leu Asn Leu Asp Thr	
260 265 270	
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Leu Gln Gln Ile Leu Lys Glu Lys Ile Ala Ser Glu Arg Phe Leu Leu	
275 280 285	
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Val Leu Asp Asp Val Trp Ser Glu Asn Arg Asp Asp Trp Glu Arg Leu	
290 295 300	
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Cys Ala Pro Leu Arg Phe Ala Ala Arg Gly Ser Lys Val Ile Val Thr	

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act cga gac aca aag att gcc agc atc att ggc aca atg aag gaa att				1008
Thr Arg Asp Thr Lys Ile Ala Ser Ile Ile Gly Thr Met Lys Glu Ile				
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Ser Leu Asp Gly Leu Gln Asp Asp Ala Tyr Trp Glu Leu Phe Lys Lys				
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Cys Ala Phe Gly Ser Val Asn Pro Gln Glu His Leu Glu Leu Glu Val				
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Lys Thr Leu Gly Ser Leu Leu Arg Leu Asp Val Ser Gln Glu His Trp				
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Arg Thr Ile Met Glu Ser Glu Val Trp Gln Leu Pro Gln Ala Glu Asn				
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Glu Ile Leu Pro Val Leu Trp Leu Ser Tyr Gln His Leu Pro Gly His				
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Leu Arg Gln Cys Phe Ala Phe Cys Ala Val Phe His Lys Asp Tyr Leu				
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ttc tat aaa cat gag ttg atc cag act tgg att gca gaa ggc ttc att				1392
Phe Tyr Lys His Glu Leu Ile Gln Thr Trp Ile Ala Glu Gly Phe Ile				
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gca cat caa gga aac aag agg atg gaa gat gtc gga agc agc tac ttc				1440
Ala His Gln Gly Asn Lys Arg Met Glu Asp Val Gly Ser Ser Tyr Phe				
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cat gag ctt gtt aat agg tct ttc ttt cag gaa tct cgg tgg aga ggg				1488
His Glu Leu Val Asn Arg Ser Phe Phe Gln Glu Ser Arg Trp Arg Gly				
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cga tat gtg atg cat gac ctc ata cac gat ctt gcc caa ttt ata tca				1536
Arg Tyr Val Met His Asp Leu Ile His Asp Leu Ala Gln Phe Ile Ser				
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Val Gly Glu Cys His Arg Ile Asp Asp Asp Lys Ser Lys Glu Thr Pro				
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agt acg act cgt cat cta tca gta gca tta act gag caa atg aag ttg				1632
Ser Thr Thr Arg His Leu Ser Val Ala Leu Thr Glu Gln Met Lys Leu				
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Gln	Arg	Asn	Gln	Tyr	Pro	Tyr	Met	Thr	Lys	Val	Asn	Ser	Cys	Leu	Leu	
565			570			575										
cct	cat	agc	ttg	ttc	aaa	aga	ctg	aaa	aga	atc	cat	gtt	tta	gtt	ttg	1776
Pro	His	Ser	Leu	Phe	Lys	Arg	Leu	Lys	Arg	Ile	His	Val	Leu	Val	Leu	
580			585			590										
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Gln	Lys	Cys	Gly	Met	Lys	Glu	Leu	Pro	Asp	Ile	Ile	Gly	Asp	Leu	Ile	
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Gln	Leu	Arg	Tyr	Leu	Asp	Ile	Ser	Tyr	Asn	Ala	Cys	Ile	Gln	Arg	Leu	
610			615			620										
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Pro	Glu	Ser	Leu	Cys	Asp	Leu	Tyr	Asn	Leu	Gln	Ala	Leu	Arg	Leu	Trp	
625			630			635			640							
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Gly	Cys	Gln	Leu	Arg	Ser	Phe	Pro	Gln	Gly	Met	Ser	Lys	Leu	Ile	Asn	
645			650			655										
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660			665			670										
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675			680			685										
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725			730			735										
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Glu	Leu	Glu	Trp	Ala	Ala	Gly	Gln	Val	Ser	Ser	Leu	Glu	His	Glu	Leu	
740			745			750										
ctt	gtc	tcg	gag	gaa	gta	ctt	tta	ggg	ctc	caa	cca	cat	cac	ttc	ctc	2304
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785 790 795 800	
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Lys Val Leu His Met Lys Arg Met Pro Val Val Lys Gln Met Ser His	
820 825 830	
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Glu Leu Cys Gly Cys Thr Lys Ser Lys Leu Phe Pro Arg Leu Glu Glu	
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Leu Val Leu Glu Asp Met Pro Thr Leu Lys Glu Phe Pro Asn Leu Ala	
850 855 860	
caa ctt cct tgt ctc aag att att cac atg aag aac atg ttt gca gta	2640
Gln Leu Pro Cys Leu Lys Ile Ile His Met Lys Asn Met Phe Ala Val	
865 870 875 880	
aaa cat ata ggt cgt gaa tta tat ggt gat ata gag agc aat tgt ttt	2688
Lys His Ile Gly Arg Glu Leu Tyr Gly Asp Ile Glu Ser Asn Cys Phe	
885 890 895	
cta tca tta gaa gag ctt gtg ctg cag gac atg ctg aca ttg gag gaa	2736
Leu Ser Leu Glu Glu Leu Val Leu Gln Asp Met Leu Thr Leu Glu Glu	
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ctc cca aat ctt gga caa ctt cca cat ctt aag gtt att cac atg aag	2784
Leu Pro Asn Leu Gly Gln Leu Pro His Leu Lys Val Ile His Met Lys	
915 920 925	
aac atg tct gca ctg aaa ctt ata ggt cgt gaa tta tgt gat tct aga	2832
Asn Met Ser Ala Leu Lys Leu Ile Gly Arg Glu Leu Cys Asp Ser Arg	
930 935 940	
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Glu Lys Ile Trp Phe Pro Arg Leu Glu Val Leu Val Leu Lys Asn Met	
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980 985 990	
agg aat aaa tgg ttt cca agg ctg gaa gag cta gaa atc aag ggc atg	3024

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Lys	Val	Phe	Arg	Ile	Lys	Gly	Leu	Pro	Ala	Val	Lys	Lys	Ile	Gly		
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Ser	Trp	Ala	Glu	Arg	Glu	Glu	Leu	Phe	Ser	Cys	Leu	Cys	Arg	Leu		
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1100		1105					1110									
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Thr	Ala	Ser	Leu	Ser	Leu	Leu	His	Ile	Ile	Lys	Cys	Pro	Asn	Leu		
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Asn	Ala	Ile	Arg	Ile	Trp	Glu	Cys	Ala	Glu	Leu	Leu	Trp	Leu	Pro		
1160		1165					1170									
gtc	aag	agg	ttt	aga	gaa	ttc	acc	acc	ctt	gag	aac	ttg	tca	ata		3564
Val	Lys	Arg	Phe	Arg	Glu	Phe	Thr	Thr	Leu	Glu	Asn	Leu	Ser	Ile		
1175		1180					1185									
agg	aac	tgc	ccc	aag	ctc	atg	agc	atg	aca	cag	tgt	gag	gag	aat		3609
Arg	Asn	Cys	Pro	Lys	Leu	Met	Ser	Met	Thr	Gln	Cys	Glu	Glu	Asn		
1190		1195					1200									
gac	ctc	ctc	ctc	ccg	ccg	tta	atc	aag	gca	cta	gaa	ttg	ggt	gac		3654
Asp	Leu	Leu	Leu	Pro	Pro	Leu	Ile	Lys	Ala	Leu	Glu	Leu	Gly	Asp		

1205

1210

1215

tgt gga aat ctt ggg aaa tcg ctg cct gga tgc cta